

## ABSTRACT OF THE DISCLOSURE

The present invention provides a method for determining amino acid sequences of peptides involving the use of a mass spectrometer that not only offers a high decomposition efficiency into fragment ions and a high selectivity of cleavage sites for a wide variety of peptide including peptides of unknown identity, but also achieves highly sensitive, high-throughput detection of the resulting fragment ions. A method for determining amino acid sequence of a peptide, comprising the steps of: preparing a peptide of interest or fragments thereof obtained by optionally cleaving the peptide of interest; coupling an amino acid derivative to the N-terminus of the peptide of interest or the fragments thereof, the amino acid derivative having protected an amino group with a protective group and derived from an amino acid with a side chain containing an acidic group; and subjecting the coupled product to mass spectrometry analysis.